

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Sherman M. Weissman Namadev Baskaran
- (ii) TITLE OF INVENTION: Amplification of Nucleic Acids
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
 - (B) STREET: 1111 Pennsylvania Ave., NW
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: Patentin Release #1.0. Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 10/073,353
 - (B) FILING DATE: 2002-02-13
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/758,662
 - (B) FILING DATE: 1996-12-07
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/758,662 (CPA)
 - (B) FILING DATE: 1999-02-17
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/585,437
 - (B) FILING DATE: 2000-06-02
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Michael S. Tuscan
 - (B) REGISTRATION NUMBER: 43,210
 - (C) REFERENCE/DOCKET NUMBER: 44921-5007-03-US
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-739-3000
 - (B) FAX: 202-739-3001
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: CGCCAGGGTT TTCCCAGTCA CGAC
- (2) INFORMATION FOR SEQ ID NO:2:

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(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: AGCGGATAAC AATTTCACAC AGGA

SCGGATAAC AATTTCACAC AGGA

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACTACGAGG GGTGTTCCCC AAAGAGCCAT GAACTGTAGA GGAAGAGAAA AAGTTCAGAG CTAAGGGCTC AGGAGATCCT GTGTATTTAG GGAAGGTGAC GGTCCAATTG GGGCCCGTTT TAGCTGCACT CACCTCTCC GGTGGCTCCT CTGGTTTCCT TCTCCAGCAG CTCCCCCATC TCAGCGGGGG CCATCCCCCT GGGAGGGAGA ACAAGGGACA GGAGGGCTGG TCAGCCCAGT AGAGAGTTGG GGGGTCCAG ATGCCTGGC CCTGGGAAGA GAGAGTAGGC TCCGGGGCCT ACCTCTTCCT CTGGCCCTTC CGCGGCCTCG GCTGCCCGGA GCCGCACAAC CCTCCCCGGG	120 180 240
CACTACGAGG GGTGTTCCCC AAAGAGCCAT GAACTGTAGA GGAAGAGAAA AAGTTCAGAG CTAAGGGCTC AGGAGATCCT GTGTATTTAG GGAAGGTGAC GGTCCAATTG GGGCCCGTTT TAGCTGCACT CACCTCTCC GGTGGCTCCT CTGGTTTCCT TCTCCAGCAG CTCCCCCATC TCAGCGGGGG CCATCCCCCT GGGAGGGAGA ACAAGGGACA GGAGGGCTGG TCAGCCCAGT AGAGAGTTGG GGGGTCCAGG ATGCCTGGGC CCTGGGAAGA GAGAGTAGGC TCCGGGGCCT ACCTCTTCCT CTGGCCCTC CGCGGCCTCG GCTGCCCGGA GCCGCACAAC CCTCCCCGGG	
CTAAGGGCTC AGGAGATCCT GTGTATTTAG GGAAGGTGAC GGTCCAATTG GGGCCCGTTT TAGCTGCACT CACCTCTCT GGTGGCTCCT CTGGTTTCCT TCTCCAGCAG CTCCCCCATC TCAGCGGGGG CCATCCCCCT GGGAGGGAG ACAAGGGACA GGAGGGCTGG TCAGCCCAGT AGAGAGTTGG GGGGTCCAGG ATGCCTGGC CCTGGGAAGA GAGAGTAGGC TCCGGGGCCT ACCTCTTCCT CTGGCCCTTC CGCGGCCTCG GCTGCCCGGA GCCGCACAAC CCTCCCCGGG	240
TAGCTGCACT CACCTCTCC GGTGGCTCCT CTGGTTTCCT TCTCCAGCAG CTCCCCCATC TCAGCGGGGG CCATCCCCCT GGGAGGGAG ACAAGGGACA GGAGGGCTGG TCAGCCCAGT AGAGAGTTGG GGGGTCCAGG ATGCCTGGGC CCTGGGAAGA GAGAGTAGGC TCCGGGGCCT ACCTCTTCCT CTGGCCCTTC CGCGGCCTCG GCTGCCCGGA GCCGCACAAC CCTCCCCGGG	
TCAGCGGGGG CCATCCCCT GGGAGGGGAG ACAAGGGACA GGAGGGCTGG TCAGCCCAGT AGAGAGTTGG GGGGTCCAGG ATGCCTGGGC CCTGGGAAGA GAGAGTAGGC TCCGGGGCCT ACCTCTTCCT CTGGCCCTTC CGCGGCCTCG GCTGCCCGGA GCCGCACAAC CCTCCCCGGG	300
AGAGAGTTGG GGGGTCCAGG ATGCCTGGGC CCTGGGAAGA GAGAGTAGGC TCCGGGGCCT ACCTCTTCCT CTGGCCCTTC CGCGGCCTCG GCTGCCCGGA GCCGCACAAC CCTCCCCGGG	360
ACCTCTTCCT CTGGCCCTTC CGCGGCCTCG GCTGCCCGGA GCCGCACAAC CCTCCCCGGG	420
GGGGTT1100 GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	480
CCCCATA ATC COTCOTTOAT AACCOTTOCT CTCCCTATA CTCCCTATA CCCCCATA	540
CCGCATAATC CCTCCTTGAT GACCCTCCCT CTCGGTAGTA CCCGCACTCT GGGGCCGAGA	600
GAAGAGGAGG GGGCACGGAC TCTTGGGGGG GGCCTCCGAG CCCGGCCCCG CCCCTCTCCC	660
CGGCTGCACG CGCCGATACC CTTTGTACCC AGGCGCGGGA CCCGGACAAT CCTCAGATCC	720
TCCAGCACCC GCTGCCCCCC AGCCCGGTGG ACGGCCCCTC GTGCCCCTCA CGCGTGCTCC	780
TGGGGCCCCG GCGCCCGTCG CCCAGTGCGG GCAGGCCGGC GGCTGCACGC GCGCCTCCGT	840
GCCCACTCCC CCCACCTCCC ACACCCTGGT CCCCTCATCC GCCCCCGGTG CTGGCCCCCT	900
GGATTGCTGC AAGTCCCGCC CGGCCCCCGG CCCCGTTGCA CCCCCGGAGC ATTGCACGGC	960
GCTTCCCCCG GGGGCGCGC CGGGCATGCA CCCGCCTCTC CCCCTCCCTT CCGCACCTCG 1	020
GCGGCCGCCG CCGCTGCAGC TCCCGCCGCC GCCGCCATCG CGCTTGCGCT GGGGGCCGAG 1	080
CCGGCGCGCG GCCGCCCCGG GTCACGTGGG CGAGGGAGGG AGGGCGAGGA GGAGCCTTAA 1	140
	200
ACTGTCCTAA GCTGGGAGCT GCAAGGGAGA ATTCCTGTCA TTCCTGGCCT CAGTTCTGCA 1:	260
	320
AGGTAACAAG CGGACGTTCT GAACTTCTCG GCTCTCGGCA GCGGCTGTAT TTCCTCTGGC 1:	380
CTGGTTGGGC TTTTCCCGCC TCTGGTTGCT TTTCTGCCTT TCTAGTTTTT GGGTTACCAG 1	440
ATAGAAGGCT TGGCCTCAGT TTTGGCCTCG CCTTTTTGCT CTTTCTAACG AGCACGAAGG 19	500
	560
GGCGTGTTAC ACCTTCACAC GCACTAGGAT CC	620

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGAGGCCATC	CGGCGGGCCT	GCCTGCCCAC	GCCGCCGCTG	CAGAGCAACC	TCTTCGCCAG	60
					TCGCCGTGTC	120
CCAGGGCAAG	AGCCATCCTT	TCAAGCCGGA	CGCCACGTAC	CACACGATGA	ACAGCGTGCC	180
		TGCCTCTGGC				240
GGCGCTCGAA	CCCGGCGATC	TGCTGGACCA	CATCTCCTCG	CCGTCGCTCG	CGCTCATGGC	300
		CGGCGGCCGG				360
CGGTGGCGGC	CCGGGCGGCG	GCGGCGGCCC	GGGCGGCGGC	GGCCCCGGGG	GAGGCGGCGG	420

TGGCGGCCCG GGGGGCGCG GCGCGGCGCG CTCCTGGGCG GCTCCGCGCA CCCTCACCCG CATATGCACA GCCTGGGCCA CCTGTCGCAC CCCGCGGCGG	480 530
(2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 515 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: ATGGCGATAA CAGTCATGTG GAGATGAAAC TTGCTGTAGA TGAAGAAGAA AATGCTGACA	60
ATAACACAAA GGCCAATGTC ACAAAACCAA AAAGGTGTAG TGGAAGTATC TGCTATGGGA CTATTGCTGT GATCGTCTTT TTCTTGATTG GATTTATGAT TGGCTACTTG GGCTATTGTA AAGGGGTAGA ACCAAAAACT GAGTGTGAGA GACTGGCAGG AACCGAGTCT CCAGTGAGGG AGGAGCCAGG AGAGGACTTC CCTGCAGCAC GTCGCTTATA TTGGGATGAC CTGAAGAGAA AGTTGTCGGA GAAACTGGAC AGCACAGACT TCACCAGCAC CATCAAGCTG CTGAATGAAA ATTCATATGT CCCTCGTGAG GCTGGATCTC AAAAAGATGA AAATCTTGCG TTGTATGTTG	120 180 240 300 360 420
AAAATCAATT TCGTGAATTT AAACTCAGCA AAGTCTGGCG TGATCAACAT TTTGTTAAGA TTCAGGTCAA AGACAGCGCT CAAAACTCGG TGATC	480 515
(2) INFORMATION FOR SEQ ID NO:6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6: GCTCAGCTCC GTTTCGGTTT CACTTCCGGT	30
(2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: AGCCCCGCAC TTCCACCACC AGCTCCTCCA	30
(2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2584 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: GAGGAGCAGC GAGTCAAGAT GAGAGTTCAG CCGCGGCGGC AGCAGCAGCA GACTCAAGAA	
TGAACAATCC GTCAGAAACC AGTAAACCAT CTATGGAGAG TGGAGATGGC AACACAGGCA	60 120
CACAAACCAA TGGTCTGGAC TTTCAGAAGC AGCCTGTGCC TGTAGGAGGA GCAATCTCAA	180
CAGCCCAGGC GCAGGCTTTC CTTGGACATC TCCATCAGGT CCAACTCGCT GGAACAAGTT	240
TACAGGCTGC TGCTCAGTCT TTAAATGTAC AGTCTAAATC TAATGAAGAA TCGGGGGATT	300
CGCAGCAGCC AAGCCAGCCT TCCCAGCAGC CTTCAGTGCA GGCAGCCATT CCCCAGACCC	360
AGCTTATGCT AGCTGGAGGA CAGATAACTG GGCTTACTTT GACGCCTGCC CAGCAACAGT TACTACTCCA GCAGGCACAG GCACAGGCAC AGCTGCTGGC TGCTGCAGTG CAGCAGCACT	420
CCGCCAGCCA GCAGCACAG GCACAGGCAC AGCTGCTGGC TGCTGCAGTG CAGCAGCACT	480 540
TGACGCAGAT CCCCCTGTCT CAGCCCATAC AGATCGCACA GGATCTTCAA CAACTGCAAC	600
AGCTTCAACA GCAGAATCTC AACCTGCAAC AGTTTGTGTT GGTGCATCCA ACCACCAATT	660
TGCAGCCAGC GCAGTTTATC ATCTCACAGA CGCCCCAGGG CCAGCAGGGT CTCCTGCAAG	720

	CGCAAAATCT	TCAAACGCAA	CTACCTCAGC	AAAGCCAAGC	CAACCTCCTA	CAGTCGCAGC	780
	CAAGCATCAC	CCTCACCTCC	CAGCCAGCAA	CCCCAACACG	CACAATAGCA	GCAACCCCAA	840
	TTCAGACACT	TCCACAGAGC	CAGTCAAÇAC	CAAAGCGAAT	TGATACTCCC	AGCTTGGAGG	900
	AGCCCAGTGA	CCTTGAGGAG	CTTGAGCAGT	TTGCCAAGAC	CTTCAAACAA	AGACGAATCA	960
-	AACTTGGATT	CACTCAGGGT	GATGTTGGGC	TCGCTATGGG	GAAACTATAT	GGAAATGACT	1020
	TCAGCCAAAC	TACCATCTCT	CGATTTGAAG	CCTTGAACCT	CAGCTTTAAG	AACATGTGCA	1080
	AGTTGAAGCC	ACTTTTAGAG	AAGTGGCTAA	ATGATGCAGA	GAACCTCTCA	TCTGATTCGT	1140
	CCCTCTCCAG	CCCAAGTGCC	CTGAATTCTC	CAGGAATTGA	GGGCTTGAGC	CGTAGGAGGA	1200
	AGAAACGCAC	CAGCATAGAG	ACCAACATCC	GTGTGGCCTT	AGAGAAGAGT	TTCTTGGAGA	1260
	ATCAAAAGCC	TACCTCGGAA	GAGATCACTA	TGATTGCTGA	TCAGCTCAAT	ATGGAAAAAG	1320
	AGGTGATTCG	TGTTTGGTTC	TGTAACCGCC	GCCAGAAAGA	AAAAAGAATC	AACCCACCAA	1380
	GCAGTGGTGG	GACCAGCAGC	TCACCTATTA	AAGCAATTTT	CCCCAGCCCA	ACTTCACTGG	1440
	TGGCGACCAC	ACCAAGCCTT	GTGACTAGCA	GTGCAGCAAC	TACCCTCACA	GTCAGCCCTG	1500
	TCCTCCCTCT	GACCAGTGCT	GCTGTGACGA	ATCTTTCAGT	TACAGGCACT	TCAGACACCA	1560
	CCTCCAACAA	CACAGCAACC	GTGATTTCCA	CAGCGCCTCC	${\tt AGCTTCCTCA}$	GCAGTCACGT	1620
	CCCCCTCTCT	GAGTCCCTCC	CCTTCTGCCT	CAGCCTCCAC	CTCCGAGGCA	TCCAGTGCCA	1680
	GTGAGACCAG	CACAACACAG	ACCACCTCCA	CTCCTTTGTC	CTCCCCTCTT	GGGACCAGCC	1740
	AGGTGATGGT	GACAGCATCA	GGTTTGCAAA	CAGCAGCAGC	TGCTGCCCTT	CAAGGAGCTG	1800
	CACAGTTGCC	AGCAAATGCC	AGTCTTGCTG	CCATGGCAGC	TGCTGCAGGA	CTAAACCCAA	1860
	GCCTGATGGC	ACCCTCACAG	TTTGCGGCTG	GAGGTGCCTT	ACTCAGTCTG	AATCCAGGGA	1920
						ACTATTCAAG	1980
	CTCTTGCTTC	TGGTGGCTCT	CTTCCAATAA	CATCACTTGA	TGCAACTGGG	AACCTGGTAT	2040
	TTGCCAATGC	GGGAGGAGCC	CCCAACATCG	TGACTGCCCC	TCTGTTCCTG	AACCCTCAGA	2100
	ACCTCTCTCT	GCTCACCAGC	AACCCTGTTA	GCTTGGTCTC	TGCCGCCGCA	GCATCTGCAG	2160
						TCCATCCAGA	2220
	ACTCTCTCTT	CACAGTGGCC	TCTGCCAGCG	GGGCTGCGTC	CACCACCACC	ACCGCCTCCA	2280
	AGGCACAGTG	AGCTGGGCAG	AGCTGGGCTG	CCAGAAGCCT	TTTTCACTCT	GCAGTGTGAT	2340
	TGGACTGCCA	GCCAGGTTAA	TAAACTGAAA	AATGTGATTG	GCTTCCTCTC	GCCGTGTTGT	2400
	GAGGGCAAAG	GAGAGAAGGG	AGAAAAAAA	AAAAAAAACC	ACACACACCC	ATACACAATA	2460
	TACCAGAAAA	GGAAGGAAGG	ATGGAGACGG	AACATTTGCC	TAATTTGTAA	TAAAACACTG	2520
	TCTTTTCAGG	GTTGCTTCAT	GGGTTGGAGG	ACTTTCTAAC	CAAAAATTAA	AAAAAAAAA	2580
	AAAA						2584

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